

This listing of claims will replace all prior versions, and listings of claims in the application.

**In the Claims:**

1. (previously presented) A method for detecting an isolate of a *B. cereus* group, in a sample, the method comprising:
  - (a) placing on a microarray of claim 10, oligonucleotide probes targeted to rRNA sequences wherein at least one mismatch is sufficient to discriminate among the *B. cereus* subgroups;
  - (b) providing conditions for hybridization of the probes with rRNA from the sample; and
  - (c) analyzing hybridization signals in the microarray from which the particular isolate is detected.
2. (previously presented) The method of claim 1, wherein the oligonucleotide probes are directed to 16S rRNA and 23S rRNA.
3. (original) The method of claim 1, wherein the probes are labeled.
4. (original) The method of claim 3, wherein the labels are selected from the group consisting of fluorescent dyes, radio isotopes, immunological labels, immuno-chemical labels and gold particles.
5. (previously presented) The method of claim 1, wherein the oligonucleotide probes discriminate one or more subgroups Anthracis, Cereus A, Cereus B, Thuringiensis A, Thuringiensis B, Mycoides A and Mycoides B.
6. (currently amended) The method of claim 1, wherein pairs of oligonucleotide probes that discriminate subgroups *Anthraxis* from *Cereus A* are ps21 (SEQ ID NO: 90)/ps22 (SEQ ID NO: 91).
7. (currently amended) The method of claim 1, wherein a ratio of hybridization signals of oligonucleotide probes ps17 (SEQ ID NO: 86) and ps18 (SEQ ID NO: 87) discriminates between *B. anthracis* Ames and *B. cereus* 9620.

8. (currently amended) The method of claim 1, wherein the oligonucleotide probes ps21 (SEQ ID NO: 90) and ps22 (SEQ ID NO: 91) discriminate *B. anthracis* Sterne from *B. cereus* HER 1414 and *B. thuringensis* B8.

9. (withdrawn) The method of claim 1, wherein the oligonucleotide probes are ps7, ps8, and ps9 to discriminate *B. thuringensis* 4Q281 from other *B. cereus* subgroup isolates.

10. (currently amended) A microarray comprising an oligonucleotide probe comprising the sequence set forth in SEQ ID NO: 143, wherein the microarray further comprises one or more that comprises oligonucleotide probes selected from the group consisting of sequences SEQ ID NOS: 70-95 and 126-175.

Oligonucleotide Name	5'-to 3'-Sequence
ps5	<del>CCG CTA ACT TCA TAA GAG CA</del> (SEQ ID NO: 74)
ps6	<del>CCG CTA ACT TCA TGA GAG CA</del> (SEQ ID NO: 75)
ps17	<del>TCT AGG GTT GTC AGA GGA TG</del> (SEQ ID NO: 86)
ps18	<del>TCT AGG GTT CTC AGA GGA TG</del> (SEQ ID NO: 87)
ps19	<del>TCT GCT CCC GAA GGA GAA GC</del> (SEQ ID NO: 88)
ps20	<del>TCT GCG CCC GAA GGA GAA GC</del> (SEQ ID NO: 89)
ps21	<del>CAG CTC AGC CTT CAC GAT AA</del> (SEQ ID NO: 90)
ps22	<del>CAG CTC AGC CTT TAC GAT AA</del> (SEQ ID NO: 91)
23F1	TTT GGG CTA TGT TCC GTT TC (SEQ ID NO: 126) and
23F2	TTT GGG CTA GAT TCC GTT TC (SEQ ID NO: 127)
A8	CCC TCT GTG ACG AGC CTT TC (SEQ ID NO: 143)

11. (currently amended) The microarray of claim 10, wherein the oligonucleotides are arranged in a specific pattern wherein I, II, III and IV are columns and A, B, C, D, E, and F are rows in the microarray:

	I	II	III	IV
A	ps19 (SEQ ID NO: 88)	ps20 (SEQ ID NO: 89)	(SEQ ID NO: 76)	(SEQ ID NO: 77)
B	(SEQ ID NO: 84)	(SEQ ID NO: 85)	(SEQ ID NO: 72)	(SEQ ID NO: 73)
C	(SEQ ID NO: 78)	(SEQ ID NO: 79)	ps5 (SEQ ID NO: 74)	ps6 (SEQ ID NO: 75)
D	(SEQ ID NO: 82)	(SEQ ID NO: 83)	(SEQ ID NO: 70)	(SEQ ID NO: 71)
E	(SEQ ID NO: 80)	(SEQ ID NO: 81)		
F	(SEQ ID NO: 142)	(SEQ ID NO: 143)	ps17 (SEQ ID NO: 86)	ps18 (SEQ ID NO: 87)

12. (currently amended) A microarray as in claim 10, wherein the oligonucleotides are arranged in pairs: ps19 (SEQ ID NO: 88) and ps20 (SEQ ID NO: 89); ps5 (SEQ ID NO: 74) and ps6 (SEQ ID NO: 75); ps17 (SEQ ID NO: 86) and ps18 (SEQ ID NO: 87).

13. (canceled).

14. (canceled).

15. (canceled).

16. (currently amended) An oligonucleotide A probe comprising the sequence of SEQ ID NO: 143, selected from the group consisting of sequences designated:

Oligonucleotide Name	5' to 3' Sequence
ps5	<del>CCG CTA ACT TCA TAA GAG CA</del> (SEQ ID NO: 74)
ps6	<del>CCG CTA ACT TCT TGA GAG CA</del> (SEQ ID NO: 75)
ps17	<del>TCT AGG GTT GTC AGA GGA TG</del> (SEQ ID NO: 86)
ps18	<del>TCT AGG GTT CTC AGA GGA TG</del> (SEQ ID NO: 87)
ps19	<del>TCT GCT CCC GAA GGA GAA GC</del> (SEQ ID NO: 88)
ps20	<del>TCT GCT CCC GAA GGA GAA GC</del> (SEQ ID NO: 89)
ps21	<del>CAG CTC AGC CTT CAC GAT AA</del> (SEQ ID NO: 90)
ps22	<del>CAG CTC AGC CTT CAC GAT AA</del> (SEQ ID NO: 91)
	TTT GGG CTA TGT TCC GTT TC (SEQ ID NO: 126)
	TTT GGG CTA GAT TCC GTT TC (SEQ ID NO: 127) and
A8	CCC TCT GTG ACG AGC CTT TC (SEQ ID NO: 143).

17. (currently amended) An isolated oligonucleotide The probe of claim 16, wherein the comprising the sequence of SEQ ID NO: 143, the oligonucleotide probe is the full reverse complement of a sequence of claim 16.

18. (canceled).

19. (canceled).

20. (currently amended) A diagnostic kit to detect *B. anthracis* target rRNA in a sample, the diagnostic kit comprising the microarray of claim 10, :

- (a) ~~a microchip that comprises at least one oligonucleotide probe that distinguishes *B. anthracis* from other closely related microorganisms, wherein the oligonucleotide is selected from the group consisting of~~

~~CCG CTA ACT TCA TAA GAG CA (SEQ ID NO: 74);~~  
~~CCG CTA ACT TCT TGA GAG CA (SEQ ID NO: 75);~~  
~~TCT AGG GTT GTC AGA GGA TG (SEQ ID NO: 86);~~  
~~TCT AGG GTT TTC AGA GGA TG (SEQ ID NO: 87);~~  
~~TCT GCT CCC GAA GGA GAA GC (SEQ ID NO: 88);~~  
~~TCT GCG CCC GAA GGG GAA GC (SEQ ID NO: 89);~~  
~~CAG CTC AGC CTT CAC GAT AA (SEQ ID NO: 90);~~  
~~CAG CTC AGC CTT TAC GAT AA (SEQ ID NO: 91);~~  
~~TTT GGG CTA TGT TCC GTT TC (SEQ ID NO: 126);~~  
~~TTT GGG CTA GAT TCC GTT TC (SEQ ID NO: 127);~~  
~~CCC TCT GTG ACG AGC CTT TC (SEQ ID NO: 143); and~~

- (b) a method for detecting hybridization between the at least one probe and the target rRNA by which hybridization, *B. anthracis* is detected.

21. (currently amended) A method for taxonomically classifying *B. cereus* groups, said method comprising:

- (a) developing strain- and subgroup-specific signature profiles of 16S and 23S rRNA sequences for *B. cereus* group isolates including subgroup *Mycoides B.* wherein the *Mycoides B.* subgroup is differentiated by SEQ ID NO: 143 from other subgroups; and
- (b) using the signature profiles to construct phylogenetic trees in order to classify the various *B. cereus* group isolates.

22. (canceled).